



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 102297

TO: Phillip Gabel
Location: 8b03 / 9e12
Tuesday, August 26, 2003
Art Unit: 1644
Phone: 308-3997
Serial Number: 09 / 454651

From: Jan Delaval
Location: Biotech-Chem Library
CM1-1E07
Phone: 308-4498

jan.delaval@uspto.gov

Search Notes

10229>
Delaval, Jan

From: Gambil, Phillip
Sent: Tuesday, August 26, 2003 9:27 AM
To: Delaval, Jan
Subject: 09 / 454,651 ifw amd

jan

please perform a sequence and a sequence interference search for

ussn 09/ 454,651 (ifw amd)

SEQ ID NO: 23

thanx

phillip gambil
art unit 1644
308-3997

1644 mailbox 9e12

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner #: _____ Date: _____
Art Unit _____ Phone Number 30 _____ Serial Number _____
Mail Box and Bldg Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

SEARCH REQUEST FORM
U.S. Patent and Trademark Office
Washington, D.C. 20591-0000
(202) 707-3000
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STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher <u>Jean</u> Searcher Phone # <u>44498</u>	NA Sequence (#) <input checked="" type="checkbox"/>	STN _____
Searcher Location <u>8126103</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Date Searcher Rec'd <u>8/26/03</u>	Structure (#) <input type="checkbox"/>	Questel Online _____
Date Input <u>8/26/03</u>	Bibliographic <input type="checkbox"/>	PTABnet _____
Searcher Prep & Rec'd Time _____	Litigation <input type="checkbox"/>	Lexis/Nexis _____
Clerks Prep Time <u>10</u>	Full Text <input type="checkbox"/>	Sequence Systems <input checked="" type="checkbox"/>
Rec'd Time <u>20</u>	Patent Family <input type="checkbox"/>	WWW Internet _____
	Other <input type="checkbox"/>	Other _____

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:17:12 ; Search time: 23 Seconds
(without alignments)
441.642 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVHVTKEYKEVA.....LVRNOTFFNNNTTKOEHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.1*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	1149	100.0	288	1	CD80 HUMAN	P33681 homo sapien
2	738	64.2	299	1	CD80 RABBIT	P42070 oryctolagus
3	561	48.8	306	1	CD80_MOUSE	Q00609 mus musculus
4	182	45.8	329	1	CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1	ICOL_HUMAN	P75144 homo sapien
6	152	13.2	309	1	CD86_MOUSE	P42082 mus musculus
7	150.5	13.1	322	1	ICOL_MOUSE	Q5jhj8 mus musculus
8	140.5	12.2	326	1	CD86_RABBIT	P42071 oryctolagus
9	138	12.0	509	1	SHSL1_RAT	P97710 r protein-t
10	134.5	11.7	583	1	CL166_MOUSE	Q61490 mus musculus
11	133.5	11.6	583	1	C1166_HUMAN	Q13740 homo sapien
12	129	11.2	221	1	BPF1_EBV	P03228 Epstein-Barr
13	127	11.1	526	1	BUTY_HUMAN	Q13410 homo sapien
14	122.5	10.7	588	1	CL166_CHICK	P42292 gallus gallus
15	120.5	10.5	513	1	SHSL1_MOUSE	P97797 m protein-t
16	120	10.4	506	1	SHSL1_BOVIN	Q46631 bos taurus
17	119	10.4	524	1	BUTY_MOUSE	Q62556 mus musculus
18	116.5	10.1	1088	1	NCAL1_XENLA	P16170 xenopus lae
19	115	10.0	761	1	NCAL2_HUMAN	P13592 homo sapien
20	115	10.0	848	1	NCAL1_HUMAN	P13591 homo sapien
21	110.5	9.6	321	1	TCB_FLY	P11364 feline leuk
22	110	9.6	398	1	SRBL1_HUMAN	Q00241 homo sapien
23	109.5	9.5	833	1	MU16_BOVIN	P43121 homo sapien
24	109.5	9.5	833	1	NCAL1_BOVIN	P31836 bos taurus
25	109	9.5	387	1	SRBL2_HUMAN	Q9P1w8 homo sapien
26	109	9.5	2029	1	LAR_DROME	P18892 bos taurus
27	109	9.5	2029	1	SRBL1_HUMAN	P16621 drosophila
28	108.5	9.4	365	1	CLXAR_MOUSE	P97792 mus musculus
29	107.5	9.4	333	1	AMAL_DROME	P15364 drosophila
30	106.5	9.3	858	1	NCAL1_RAT	P13596 rattus norvegicus
31	105	9.1	319	1	A33_HUMAN	Q97959 homo sapien
32	105	9.1	1091	1	NCAL1_CHICK	P13590 gallus gallus
33	104	9.1	1092	1	NCAL2_XENLA	P363335 xenopus lae

ALIGNMENTS

34	103.5	9.0	725	1	NCA2_MOUSE	P13594 mus musculus
35	103.5	9.0	1115	1	NCAL1_MOUSE	P13395 mus musculus
36	103	9.0	298	1	JAM2_HUMAN	P57087 homo sapien
37	102.5	8.9	503	1	SHS1_HUMAN	P78224 h protein-t
38	102	8.9	1443	1	NEO1_CHICK	Q90110 gallus gallus
39	101.5	8.8	403	1	RAGE_MOUSE	P62151 mus musculus
40	100	8.7	413	1	MEMO1_HUMAN	P31398 manduca sexta
41	99.5	8.7	1338	1	VGR1_HUMAN	P17488 h vascular
42	98.5	8.6	365	1	CXAR_HUMAN	P78110 homo sapien
43	98.5	8.6	1242	1	NPNN_MOUSE	P9qg57 mus musculus
44	98	8.5	278	1	OX2G_RAT	P04218 rattus norvegicus
45	98	8.5	298	1	JAM1_BOVIN	P9xt56 bos taurus

RESULT 1						
ID	CD80_HUMAN	STANDARD	PRT;	288 AA.		
AC	P33681;					
DT	01-FEB-1994 (Rel. 28, Created)					
DT	01-FEB-1994 (Rel. 28, Last sequence update)					
DT	15-SEP-2003 (Rel. 42, Last annotation update)					
DE	T lymphocyte activation antigen CD80 precursor (Activation B7-1)					
DE	antigen) (CTLA-4 counter-receptor B7-1) (B7) (BBL)					
DE	CD80 OR CD28LG1 OR CD28LG OR LAB7.					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.					
NCBI_TaxID	95066;					
RN	SEQUENCE FROM N.A.					
RC	TISSUE=Lymphoid;					
RX	Medline=9001047; PubMed=2794510;					
RA	Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M.;					
RA	"B7", a new member of the Ig superfamily with unique expression on activated and neoplastic B cells.";					
RT	J. Immunol. 143:2714-2722(1994).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	Medline=9230753; PubMed=1377173;					
RA	Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;					
RA	"Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7.",					
RN	[3]					
RP	SEQUENCE OF 35-38.					
RX	Medline=91341422; PubMed=1711935;					
RA	Freeman G.J., Gray G.S., Gianni C.D., Lombard D.B., Zhou L., White P., Fingerot J.D., Gribben J.G., Nadler L.M.;					
RA	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.",					
RT	J. Immunol. 154:97-105(1995).					
RN	[4]					
RP	CHARACTERIZATION.					
RX	Medline=95088403; PubMed=7527824;					
RA	Lanier L.L., Fallon S., Somozza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;					
RA	"Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.",					
RL	J. Exp. Med. 174:625-631(1991).					
RN	[5]					
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.					
RX	Medline=20125021; PubMed=16661405;					
RA	Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K., Jones B.Y., Stuart D.I., Davis S.J.;					
RA	"Structure and dimerization of a soluble form of B7-1."					
RL	Immunity 12:51-60(2000)					
CC	"- PUNCTUM: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE					

PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES AND DENDRITIC CELLS.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- DATABASE: NAME=PROW; NOTE=CD28 entry; WWW="http://www.ncbi.nlm.nih.gov/protein/cd28.html".

CC -!- DATA SOURCE: NAME=CD28; NOTE=CD28 entry; WWW="http://www.ncbi.nlm.nih.gov/protein/cd28.html".

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CC -!- EMBL; M27533; AAA36045.1; -
DR EMBL; M83072; AAA8390.1; JOINED.
DR EMBL; M83073; AAA8390.1; JOINED.
DR EMBL; M83074; AAA8390.1; JOINED.
DR PIR; I54495; A45803.
DR PDB; 1DR9; 10-JAN-01.
DR Genew; HGNC:1700; CD80.
DR MIM; 112303; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SMM00409; Ig; 1.
DR PROSITE; PS50835; Ig_LIKE; 2.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;

KW Receptor; 3D-structure.

FT SIGNAL 1 34
FT CHAIN 35 288 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.

FT DOMAIN 35 242 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 243 263 POTENTIAL.
FT DOMAIN 264 288 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 35 135 IG-LIKE V-TYPE.
FT DOMAIN 145 230 IG-LIKE C2-TYPE.
FT DISULFID 50 116

FT DISULFID 162 216 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 89 89 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) .
FT CARBOHYD 207 207 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 226 226 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 232 232 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT STRAND 37 41

FT TURN 42 43

FT STRAND 46 48

FT TURN 56 57

FT HELIX 58 61

FT STRAND 63 68

FT TURN 69 70

FT STRAND 71 77

FT TURN 78 79

FT STRAND 80 83

FT HELIX 85 88

FT TURN 89 90

FT STRAND 91 94

FT TURN 96 99

FT STRAND 100 103

FT HELIX 108 110

FT STRAND 112 120

FT TURN 123 124

FT STRAND 127 139

FT STRAND 146 151

CC	SEQUENCE	288 AA;	33048 MW;	BA453EE34528B1F4	CRC64;
CC	Query Match	100.0%	Score 1149;	DB 1;	Length 288;
CC	Best Local Similarity	100.0%	Pred. No. 1.7e-88;		
CC	Matches	216	Conservative 0;	Indels 0;	Gaps 0;
QY	1	GLSHFCGTYIHTKEYKEVATLSCGHNVSEELAQTRIYQKEKVKMYLTMMMSGDMMNWIPE	60		
DB	27	GLSHFCGTYIHTKEYKEVATLSCGHNVSEELAQTRIYQKEKVKMYLTMMMSGDMMNWIPE	86		
QY	61	YKRTIFTDTNNLIVILARLPDEGTYECVILKYKEFDAFREHLAETVLSYKADDEFTPS	120		
DB	87	YKRTIFTDTNNLIVILARLPDEGTYECVILKYKEFDAFREHLAETVLSYKADDEFTPS	146		
QY	121	ISDPEIPTSNIIRRICSTSGGGFPEPHISWLWENGEELNAINNTYQDQPETELYAVSSKLDF	180		
DB	147	ISDPEIPTSNIIRRICSTSGGGFPEPHISWLWENGEELNAINNTYQDQPETELYAVSSKLDF	206		
QY	181	NMTINHSHFMCILYGHILRVNOTFNWNNTIKQEHFPDN	216		
DB	207	NMTINHSHFMCILYGHILRVNOTFNWNNTIKQEHFPDN	242		
RESULT 2					
CD80_RABBIT	STANDARD;		PRT;	299 AA.	
ID	CD80_RABBIT				
AC	P42070;				
DT	01-NOV-1995 (Rel. 32, Created)				
DT	01-NOV-1995 (Rel. 32, Last sequence update)				
DT	15-SEP-2003 (Rel. 42, Last annotation update)				
DE	T lymphocyte activation antigen CD80 precursor (Activation, B7-1 antigen).				
GN	CD80.				
OS	Oryctolagus cuniculus (Rabbit).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.				
OX	NCBI_TaxID=9886;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	STRAIN=B1J X CHBB; HM; MEDLINE=15369849; PubMed=7642234;				
RA	Isono T., Seco A.; Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules"; Immunogenetics 42:217-220 (1995).				
RT	"Cloning and sequencing of the rabbit gene encoding T-cell costimulatory molecules"; Immunogenetics 42:217-220 (1995).				
RL	CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS RECEPTOR.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.				
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	DR EMBL; D43843; BAA08643.1; -.				

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:17:57 ; Search time 96 Seconds
(without alignments)
580.618 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: I1GSHFCGSVHVTKEYKEVA.....IRVNQTFNNNTTKQEBHFPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

SPREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rdent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

Database :

2: sp_archaea:*

3: sp_bacteria:*

4: sp_fungi:*

5: sp_human:*

6: sp_invertebrate:*

7: sp_mammal:*

8: sp_mhc:*

9: sp_organelle:*

10: sp_plant:*

11: sp_rdent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

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11: sp_rdent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

1: sp_archaea:*

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3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rdent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

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1: sp_archaea:*

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12: sp_virus:*

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14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

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16: sp_bacteriaph:*

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10: sp_plant:*

11: sp_rdent:*

12: sp_virus:*

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14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

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13: sp_vertebrate:*

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15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

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14: sp_unclassified:*

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14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

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7: sp_mhc:*

8: sp_organelle:*

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7: sp_mhc:*

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9: sp_phage:*

10: sp_plant:*

11: sp_rdent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriaph:*

17: sp_archeap:*

1: sp_archaea:*

2: sp_bacteria:*

QY	122	SDFEIPTSNIRRICSTSGFPPEPHSLWLENGELNAINNTSQDPETELYAVSSKLDNF	181	RESULT 3
Db	148	TDFEPPSNIRRICSTSGFPPEPHSLWLENGELNAINNTSQDPETLYVSSKLDNF	207	Q9BDN6 PRELIMINARY; PRT; 288 AA.
QY	182	MTTNHSFMCILIKYGHLYRQNTFWNTTKOEHFPDN	216	Q9BDN6; ID Q9BDN6; AC Q9BDN6; ID Q9BDN6; PRELIMINARY; PRT; 288 AA.
Db	208	MTTNHSFMCILIKYGHLYRQNTFWNTPKQEHFPDN	242	AC Q9BDN6; ID Q9BDN6; PRELIMINARY; PRT; 288 AA.
				DT 01-JUN-2001 (TREMBLrel. 17, Created)
				DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
				DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
				DE CD80 protein.
				GN MNB71.
				OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
				OC Cercopithecinae; Cercocebus.
				OX NCBI_TaxID=5531;
				RN [1]
				SEQUENCE FROM N.A. PubMed=11491535;
				RP RX MEDLINE=21303618; PubMed=11491535;
				RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
				RT "Cloning, sequencing, and homology analysis of nonhuman primate RT Fas/Fas-ligand and co-stimulatory molecules.";
				RL Immunogenetics 52:315-328 (2001).
				EMBL: AF344839; AAC37535.1; -.
				HSSP: P33681; 1DB9.
				DR InterPro; IPR00359; Ig-like.
				DR InterPro; IPR007110; Ig-like.
				DR InterPro; IPR003006; Ig_MHC.
				DR P00047; Ig; 1.
				SMART: SM00469; Ig; 1.
				PROSITE: PS50835; Ig_LIKE; 1.
				DR PROSITE: PS50835; Ig_LIKE; 1.
				DR SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;
				Query Match 94.4%; Score 1085; DB 6; Length 288;
				Best Local Similarity 95.3%; Pred. No. 9_4e-90; Indels 0; Gaps 0; Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY	2	LSHFCGVTHVTKVKEYVATISCGHNVSYEELAQTRIYQKEKKMVLTTMSGDMNINWPEY	61	QY 2 LSHFCGVTHVTKVKEYVATISCGHNVSYEELAQTRIYQKEKKMVLTTMSGDMNINWPEY 61
Db	28	LSHFCGVTHVTKVKEYVATISCGHNVSYEELAQTRIYQKEKKMVLTTMSGDMNINWPEY	87	Db 28 LSHFCGVTHVTKVKEYVATISCGHNVSYEELAQTRIYQKEKKMVLTTMSGDMNINWPEY 87
QY	62	KNRTIDFTNNLSIVTLARPSDEGTYECVVLKYEKAFKREHLAETVLSVRADEPTPSI	121	QY 62 KNRTIDFTNNLSIVTLARPSDEGTYECVVLKYEKAFKREHLAETVLSVRADEPTPSI 121
Db	88	KNRTIDFTNNLSIVTLARPSDEGTYECVVLKYEKAFKREHLAETVLSVRADEPTPSI	147	Db 88 KNRTIDFTNNLSIVTLARPSDEGTYECVVLKYEKAFKREHLAETVLSVRADEPTPSI 147
QY	122	SDFEIPTSNIRRICSTSGFPPEPHSLWLENGELNAINNTSQDPETLYAVSSKLDNF	181	QY 122 SDFEIPTSNIRRICSTSGFPPEPHSLWLENGELNAINNTSQDPETLYAVSSKLDNF 181
Db	148	TDFEPPSNIRRICSTSGFPPEPHSLWLENGELNAINNTSQDPETLYAVSSKLDNF	207	Db 148 TDFEPPSNIRRICSTSGFPPEPHSLWLENGELNAINNTSQDPETLYAVSSKLDNF 207
QY	182	MTTNHSFMCILIKYGHLYRQNTFWNTTKOEHFPDN	216	QY 182 MTTNHSFMCILIKYGHLYRQNTFWNTTKOEHFPDN 216
Db	208	MTTNHSFMCILIKYGHLYRQNTFWNTPKQEHFPDN	242	Db 208 MTTNHSFMCILIKYGHLYRQNTFWNTPKQEHFPDN 242
				RN [1]
				SEQUENCE FROM N.A.
				RP TISSUE=Blood;
				RC MEDLINE=9603435; PubMed=7561102;
				RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
				RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates.";
				RL J. Immunol. 155:3946-3954 (1995).
				RN [2]
				RP SEQUENCE FROM N.A.
				RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
				RA Weiss W.R., Ansari A.A.;
				RT "Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-ligand and co-stimulatory molecules.";
				RL Immunogenetics 0:0-0 (2001).
				DR EMBL: U19840; AAA86706.1; -.
				DR EMBL: AF444849; AAC37609.1; -.
				DR HSSP: P33681; 1DR9.
				DR InterPro; IPR003599; Ig_Like.
				DR InterPro; IPR007110; Ig_Like.
				DR P00047; Ig; 1.
				DR SMART: SM00469; Ig; 1.
				DR PROSITE: PS50835; Ig_LIKE; 2.
				KW Signal.
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QY	2	LSHFCGVTHVTKVKEYVATISCGHNVSYEELAQTRIYQKEKKMVLTTMSGDMNINWPEY	61	RESULT 4
Db	28	LSHFCGVTHVTKVKEYVATISCGHNVSYEELAQTRIYQKEKKMVLTTMSGDMNINWPEY	87	Q2B347 PRELIMINARY; PRT; 289 AA.
QY	62	KRTIDFTNNLSIVTLARPSDEGTYECVVLKYEKAFKREHLAETVLSVKADEPTPSI	121	AC Q2B347; PRELIMINARY; PRT; 289 AA.
Db	88	KRTIDFTNNLSIVTLARPSDEGTYECVVLKYEKAFKREHLAETVLSVKADEPTPSI	147	DT 01-NOV-1996 (TREMBLrel. 01, Created)
Qy	122	SDFEIPTSNIRRICSTSGFPPEPHSLWLENGELNAINNTSQDPETLYAVSSKLDNF	181	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
Db	148	TSEIEPPSNIRRICNSGGFPPEPHSLWLENGELNAINNTSQDPETLYVSSKLDNF	207	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
Qy	182	MTTNHSFMCILIKYGHLYRQNTFWNTTKOEHFPDN	216	DE B7 protein (Fragment).
Db	208	MTTNHSFMCILIKYGHLYRQNTFWNTPKQEHFPDN	242	GN B7.
				Cercocebus torquatus (red-crowned mangabey).
				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
				OC Cercopithecinae; Cercocebus.
				OX NCBI_TaxID=5530;
				RN SEQUENCE FROM N.A.
				RC TISSUE=Blood;
				RC MEDLINE=9603435; PubMed=7561102;
				RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
				RT "Comparative sequence analysis of cytokine genes from human and

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OM protein - protein search, using sw model

Run on: August 26, 2003, 10:23:43 ; Search time 57 Seconds
(without alignments)
500.065 Million cell updates/sec

Title: US-09-454-651b-23
Perfect score: 1149
Sequence: GLSHFCGIVHVTKEYEVA.....IRVNQTFNNNTTKQEHFPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 497079 seqs, 13196178 residues

Total number of hits satisfying chosen parameters: 497079

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 100%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6_ptodata/1/pubpaas/US06_NSW_PUB.pep:/*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1 1149 100.0 226 10 US-09-915-789A-21 Sequence 21, Appl
2 1149 100.0 288 8 US-08-592-711-2 Sequence 2, Appl
3 1149 100.0 288 9 US-09-772-102-14 Sequence 14, Appl
4 1149 100.0 288 9 US-09-837-867A-19 Sequence 19, Appl
5 1149 100.0 288 10 US-09-110-174A-5 Sequence 5, Appl
6 1149 100.0 288 10 US-09-896-738-10 Sequence 10, Appl
7 1149 100.0 288 10 US-09-915-789A-15 Sequence 15, Appl
8 1149 100.0 288 11 US-09-962-367-19 Sequence 19, Appl
9 1149 100.0 288 11 US-09-350-202-12 Sequence 2, Appl
10 1149 100.0 288 12 US-10-132-214-278 Sequence 278, Appl
11 1149 100.0 288 15 US-10-261-101-2 GENERAL INFORMATION
12 1149 100.0 473 10 US-09-910-559-131 Sequence 131, Appl
13 1143 99.5 492 10 US-09-845-89A-3 Sequence 3, Appl
14 1129 98.3 288 12 US-10-032-214-94 Sequence 94, Appl
15 1121 97.6 288 12 US-10-032-214-69 Sequence 69, Appl

ALIGNMENTS

RESULT 1
US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US 2002168762A1
; GENERAL INFORMATION
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-915-789A-21

Query Match 100.0% ; Score 1149; DB 10; Length 226;
Best Local Similarity 100.0% ; Pred. No. 5.1e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGIVHVTKEYEVAATRIVQKEKRMVLTMSGDNNTWPE
Db 11 GLSHFCGIVHVTKEYEVAATRIVQKEKRMVLTMSGDNNTWPE
Qy 61 YKNRTFIDTINNLIVILARPSDEGTVCVLYKEFDAKREHLAEVTLVKADFTPTPS
Db 71 YKNRTFIDTINNLIVILARPSDEGTVCVLYKEFDAKREHLAEVTLVKADFTPTPS
Qy 121 ISDFEIPTSNTRRICSTSGFPFHLSWENGEELNANTVSDPTELYAVSSKLDF
Db 131 ISDFEIPTSNTRRICSTSGFPFHLSWENGEELNANTVSDPTELYAVSSKLDF
Qy 181 NMTTNSFMCILIKYGHLYNQTFNNNTQKEHFPDN 216

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 M protein - protein search, using sw model
 run on: August 26, 2003, 12:18:59 ; Search time 17 Seconds
 (without alignments)
 537.597 Million cell updates/sec

title: US-09-454-651B-23
 effect score: 1149
 sequence: 1 GLSHFCGVHVTKEKVA.....LKVQTNWNNTKQEHPDN 216

coring table: BLOSUM62
 Gapext 0.5
 searched: 328717 seqs, 42310858 residues

total number of hits satisfying chosen parameters: 328717

minimum DB seq length: 0
 maximum DB seq length: 2000000000

post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

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 2: /cgn2_6/prodata/1/iaa/5B_COMBO.pep:
 3: /cgn2_6/prodata/1/iaa/6A_COMBO.pep:
 4: /cgn2_6/prodata/1/iaa/6B_COMBO.pep:
 5: /cgn2_6/prodata/1/iaa/PCTUS_COMBO.pep:
 6: /cgn2_6/prodata/1/iaa/backfile1.pep:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	2 US-09-147-772-2	Sequence 2, Appli
2	1149	100.0	288	2 US-09-145-104-6	Sequence 6, Appli
3	1149	100.0	288	2 US-08-101-624-23	Sequence 23, Appli
4	1149	100.0	288	2 US-08-751-767A-6	Sequence 6, Appli
5	1149	100.0	288	3 US-08-153-62-2	Sequence 2, Appli
6	1149	100.0	288	3 US-08-419-74A-29	Sequence 29, Appli
7	1149	100.0	288	3 US-08-280-757B-29	Sequence 29, Appli
8	1149	100.0	288	3 US-09-159-135-2	Sequence 19, Appli
9	1149	100.0	288	3 US-08-205-697A-19	Sequence 19, Appli
10	1149	100.0	288	3 US-08-702-525-19	Sequence 19, Appli
11	1149	100.0	288	4 US-09-450-798-2	Sequence 2, Appli
12	1149	100.0	288	4 US-08-403-253A-2	Sequence 13, Appli
13	1149	100.0	288	4 US-09-651-200-13	Sequence 34, Appli
14	1149	100.0	288	4 US-09-66-15-14	Sequence 2, Appli
15	1149	100.0	288	4 US-08-435-816A-12	Sequence 19, Appli
16	1149	100.0	288	5 PCT-US95-0257-19	Sequence 19, Appli
17	1149	100.0	473	3 US-09-171-945-131	Sequence 131, Appli
18	1102	95.9	208	4 US-09-460-384-36	Sequence 36, Appli
19	1100	95.7	208	4 US-09-651-200-14	Sequence 14, Appli
20	1050	91.4	208	3 US-08-630-172-15	Sequence 15, Appli
21	1050	91.4	208	3 US-09-375-419-15	Sequence 15, Appli
22	743	64.7	292	4 US-09-651-200-16	Sequence 16, Appli
23	743	64.7	292	4 US-09-303-040-2	Sequence 2, Appli
24	739	64.3	292	4 US-09-303-040-4	Sequence 4, Appli
25	738	64.2	299	4 US-09-651-200-15	Sequence 15, Appli
26	561	49.8	306	3 US-09-205-97A-17	Sequence 17, Appli
27	561	48.8	306	3 US-08-702-525-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
 US-09-147-772-2
 ; Sequence 2, Application US/08147772

; Patent No. 558776

; GENERAL INFORMATION:

; APPLICANT: Ostrand, Rosenberg, Suzanne

; APPLICANT: Baskar, Sivabubramanian

; APPLICANT: Glimcher, Laurie H.

; APPLICANT: Freeman, Gordon J.

; TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 State Street, Suite 510

; CITY: Boston

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/147,772

; FILING DATE:

; CLASSIFICATION: 424

; PRIOR APPLICATION NUMBER:

; APPLICATION NUMBER:

; ATTORNEY/AGENT INFORMATION:

; NAME: Mandragours, Amy E.

; REGISTRATION NUMBER: 36,207

; REFERENCE/DOCKET NUMBER: RPI-003

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 227-7400

; TELEFAX: (617) 227-5941

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 288 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: B cell activation antigen; natural ligand

; DESCRIPTION: For CD28 T cell surface antigen; transmembrane protein

; FEATURE: signal sequence

; NAME/KEY: -34 to -1

; LOCATION: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein
 OTHER INFORMATION: hydrophobic
 FEATURE: extracellular domain
 NAME/KEY: 1 to 208
 LOCATION: 1 to 208
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: transmembrane domain
 LOCATION: 209 to 235
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: intracellular domain
 LOCATION: 236 to 254
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: N-linked glycosylation
 LOCATION: 19 to 21
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: N-linked glycosylation
 LOCATION: 55 to 57
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: N-linked glycosylation
 LOCATION: 64 to 66
 IDENTIFICATION METHOD: similarity with known sequence
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 FEATURE: NAME/KEY: N-linked glycosylation
 LOCATION: 152 to 154
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: N-linked glycosylation
 LOCATION: 173 to 175
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: N-linked glycosylation
 LOCATION: 177 to 179
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: N-linked glycosylation
 LOCATION: 193 to 200
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: Ig V-set domain
 LOCATION: 1 to 104
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 PUBLICATION INFORMATION:
 AUTHORS: FREEMAN, GORDON J.
 AUTHORS: FREEMAN, ARNOLD S.
 AUTHORS: SEGIL, JEFFREY M.
 AUTHORS: LEE, GRACE
 AUTHORS: WHITMAN, JAMES F.

IDENTIFICATION METHOD: soluble protein
 OTHER INFORMATION: hydrophobic
 FEATURE: extracellular domain
 NAME/KEY: 1 to 143
 LOCATION: 1 to 143
 IDENTIFICATION METHOD: similarity with known sequence
 IDENTIFICATION METHOD: sequence
 FEATURE: NAME/KEY: 2714-2722
 LOCATION: 2714-2722
 IDENTIFICATION METHOD: sequence
 IDENTIFICATION METHOD: sequence
 PAGES: 2714-2722
 DATE: 15-OCT-1989
 RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 US-08-147-772-2

Query Match 100.0%; Score 1149; DB: 2; Length 288;
 Best Local Similarity 100.0%; Pred. No. 7e-113;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGIVTHKEVKEVATLSCGHNVSVELAQTRIYQWKEKAVVLTMMGDMNIWPE 60
 Db 27 GLSHFCGIVTHKEVKEVATLSCGHNVSVELAQTRIYQWKEKAVVLTMMGDMNIWPE 86

Qy 61 YKRTTIFDITNNISIVILALRSPDEGTTECVVLYKEDAFKREBLAEVTLVSKADEFPPS 120
 Db 87 YKRTTIEDITNNISIVILALRSPDEGTTECVVLYKEDAFKREBLAEVTLVSKADEFPPS 146

Qy 121 ISDFRIPTSNIRRICTSGGFPPEHLSWLENGBELNAINTVSQDPETELYAVSSKLDF 180
 Db 147 ISDFRIPTSNIRRICTSGGFPPEHLSWLENGBELNAINTVSQDPETELYAVSSKLDF 206

Qy 181 NMNTNHSFENCLIKYGHLYRNTQFWNTTKQEHFPDN 216
 Db 207 NMNTNHSFENCLIKYGHLYRNTQFWNTTKQEHFPDN 242

RESULT 2
 US-08-456-104-6
 Sequence 6, Application US/08456104
 Patent No. 5861310
 GENERAL INFORMATION:
 APPLICANT: Freeman, Gordon J.
 ATTORNEY/AGENT INFORMATION:
 APPLICANT: Nadler, Lee M.
 APPLICANT: Gray, Gary S.
 TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 State Street, Suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/456,104
 FILING DATE: 19-AUG-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/101,624;
 FILING DATE: 26-JUL-1993;
 APPLICATION NUMBER: 08/109,393;
 APPLICATION NUMBER: 19-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Mandragoras, Amy E.
 REGISTRATION NUMBER: 36,207
 REFERENCE/DOCKET NUMBER: RPI-008
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 288 amino acids